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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2011; month=3; day=28; hr=12; min=13; sec=28; ms=84;]

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Reviewer Comments:

<210> 6

<211> 11

<212> PRT

<213> Unknown

<220>

<223> motif 1, found in cyclin A proteins

<220>

<221> misc_feature

<222> 3

<223> Xaa at position 3 may be Val or Ile

<220>

<221> misc_feature

<223> Xaa at position 6 may be Ser or Ala

<220>

<221> misc_feature

<222> 7

<223> Xaa at position 7 may be Asp or Glu

<220>

<221> misc_feature

<222> 8

<223> Xaa at position 8 may be Asp or Glu

<220>

<221> misc_feature

<222> 10
<223> Xaa at positon 10 may be Lys, Arg or Thr

<400> 6

Trp Leu Xaa Glu Val Xaa Xaa Xaa Tyr Xaa Leu
1 5 10

A mandatory feature is required to cover every "Xaa" used in a sequence.
SEQ ID # 6 does not have a feature to cover the "Xaa" at positions 9.
Please make all necessary changes.

<210> 13
<211> 15
<212> PRT
<213> Medicago

<220>

<400> 13

Trp Leu Val Glu Val Ser Glu Gly Tyr Lys Leu Gln Ala Asn Thr

"The enumeration of amino acids shall start at the first amino acid as
number 1. It shall be marked below the sequence every 5 amino acids."
SEQ ID# 13 and 25 is missing amino acid numbers. Please renumber SEQ ID#
13 and 25 to show the correct numbering. This error appears in many
other sequences in this sequence listing. Please make all necessary
changes.

Application No: 10584024 Version No: 3.0

Input Set:

Output Set:

Started: 2011-03-14 12:54:29.950
Finished: 2011-03-14 12:54:31.031
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 81 ms
Total Warnings: 6
Total Errors: 1
No. of SeqIDs Defined: 31
Actual SeqID Count: 31

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 341	'Xaa' position not defined SEQID (6) POS (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (25)

SEQUENCE LISTING

<110> CropDesign N.V.

<120> Plants having increased yield and method for making the same

<130> CD-106-PCT

<140> 10584024

<141> 2011-03-14

<150> US 60/532,287

<151> 2003-12-22

<160> 31

<170> PatentIn version 3.3

<210> 1

<211> 1311

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<223> A variant of the coding sequence of the sequence deposited under accession number NM_121168 contains a G instead of C on position 851 and a T instead of C on position 1295

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gtacaggaga gttttgtacg aataacgaga tcacgagcta aaaaagccat gggaagagga	120
gtatcaatac ctccaacaaa accttctttt aaacagcaaa agagacgtgc agtacttaag	180
gatgtgagta atacctctgc agatattatt tattcagaac ttcgaaaggg aggcaacatc	240
aaggcaaaca gaaaatgtct aaaagagcct aaaaaagcag caaaggaagg tgctaacagt	300
gccatggata ttctggtaga tatgcataca gaaaaatcaa aattagcaga agatttgtcc	360
aagatcagga tggctgaagc ccaagatgtc tctctttcaa actttaaaga tgaagaaatt	420
actgagcaac aagaagatgg atcaggtgtc atggagttac ttcaagttgt agatattgat	480
tccaacgtcg aagatccaca gtgttgacgc ttgtatgctg ctgatatata tgacaacata	540
catgttgacg agcttcaaca acgacccttg gctaattata tggagcttgt gcagcgagat	600
atcgaccacg acatgagaaa gattctgatt gactggcttg tagaagtttc tgacgactac	660
aagctgggtc cagatacgct ttaccttaca gtgaatctta tcgaccggtt tctgtccaac	720
agttacattg aaaggcaaag actccagctc cttggtgtct cttgcatget tatagcttca	780

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aaatatgaag agctttccgc accaggggtg gaggagtttt gcttcattac ggccaacaca      840
tacacaagac cagaagtgct gagcatggag attcaaattc taaattttgt gcactttaga      900
ttatcgggttc ctaccaccaa aacatttctg aggcgggttca ttaaagcagc tcaagcttcg      960
tacaaggtgc ctttcattga actggagtat ttagcaaact atctcgccga attgacactg     1020
gtggaatata gtttcctaag gttcctgcc aactaattg ctgcttcage tgttttccta     1080
gcccgatgga cactcgacca aactgaccat ccttgggaacc ctactctgca acactacacc     1140
agatatgagg tagctgagct gaagaacaca gttctcgcca tggaggactt gcagctcaac     1200
accagtggct gtactctcgc tgccaccgct gagaaatata accaaccaaa gtttaagagc     1260
gtggcaaagc tgacatctcc caaacgagtc acatcactat tctcaagatg a              1311

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<210>  2
<211>  436
<212>  PRT
<213>  Arabidopsis thaliana

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<220>
<221>  MISC_FEATURE
<223>  A variant of the sequence deposited under accession number
      NP_568248 contains an arginine instead of a proline on position
      284 and a phenylalanine instead of a serine on position 432

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<400>  2

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Met Tyr Cys Ser Ser Ser Met His Pro Asn Ala Asn Lys Glu Asn Ile
1              5              10              15

```

```

Ser Thr Ser Asp Val Gln Glu Ser Phe Val Arg Ile Thr Arg Ser Arg
      20              25              30

```

```

Ala Lys Lys Ala Met Gly Arg Gly Val Ser Ile Pro Pro Thr Lys Pro
      35              40              45

```

```

Ser Phe Lys Gln Gln Lys Arg Arg Ala Val Leu Lys Asp Val Ser Asn
      50              55              60

```

```

Thr Ser Ala Asp Ile Ile Tyr Ser Glu Leu Arg Lys Gly Gly Asn Ile
      65              70              75              80

```

```

Lys Ala Asn Arg Lys Cys Leu Lys Glu Pro Lys Lys Ala Ala Lys Glu
      85              90              95

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Gly	Ala	Asn	Ser	Ala	Met	Asp	Ile	Leu	Val	Asp	Met	His	Thr	Glu	Lys	100	105	110
Ser	Lys	Leu	Ala	Glu	Asp	Leu	Ser	Lys	Ile	Arg	Met	Ala	Glu	Ala	Gln	115	120	125
Asp	Val	Ser	Leu	Ser	Asn	Phe	Lys	Asp	Glu	Glu	Ile	Thr	Glu	Gln	Gln	130	135	140
Glu	Asp	Gly	Ser	Gly	Val	Met	Glu	Leu	Leu	Gln	Val	Val	Asp	Ile	Asp	145	150	155
Ser	Asn	Val	Glu	Asp	Pro	Gln	Cys	Cys	Ser	Leu	Tyr	Ala	Ala	Asp	Ile	165	170	175
Tyr	Asp	Asn	Ile	His	Val	Ala	Glu	Leu	Gln	Gln	Arg	Pro	Leu	Ala	Asn	180	185	190
Tyr	Met	Glu	Leu	Val	Gln	Arg	Asp	Ile	Asp	Pro	Asp	Met	Arg	Lys	Ile	195	200	205
Leu	Ile	Asp	Trp	Leu	Val	Glu	Val	Ser	Asp	Asp	Tyr	Lys	Leu	Val	Pro	210	215	220
Asp	Thr	Leu	Tyr	Leu	Thr	Val	Asn	Leu	Ile	Asp	Arg	Phe	Leu	Ser	Asn	225	230	235
Ser	Tyr	Ile	Glu	Arg	Gln	Arg	Leu	Gln	Leu	Leu	Gly	Val	Ser	Cys	Met	245	250	255
Leu	Ile	Ala	Ser	Lys	Tyr	Glu	Glu	Leu	Ser	Ala	Pro	Gly	Val	Glu	Glu	260	265	270
Phe	Cys	Phe	Ile	Thr	Ala	Asn	Thr	Tyr	Thr	Arg	Pro	Glu	Val	Leu	Ser	275	280	285
Met	Glu	Ile	Gln	Ile	Leu	Asn	Phe	Val	His	Phe	Arg	Leu	Ser	Val	Pro	290	295	300
Thr	Thr	Lys	Thr	Phe	Leu	Arg	Arg	Phe	Ile	Lys	Ala	Ala	Gln	Ala	Ser	305	310	315
																		320

Tyr Lys Val Pro Phe Ile Glu Leu Glu Tyr Leu Ala Asn Tyr Leu Ala
325 330 335

Glu Leu Thr Leu Val Glu Tyr Ser Phe Leu Arg Phe Leu Pro Ser Leu
340 345 350

Ile Ala Ala Ser Ala Val Phe Leu Ala Arg Trp Thr Leu Asp Gln Thr
355 360 365

Asp His Pro Trp Asn Pro Thr Leu Gln His Tyr Thr Arg Tyr Glu Val
370 375 380

Ala Glu Leu Lys Asn Thr Val Leu Ala Met Glu Asp Leu Gln Leu Asn
385 390 395 400

Thr Ser Gly Cys Thr Leu Ala Ala Thr Arg Glu Lys Tyr Asn Gln Pro
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Lys Phe Lys Ser Val Ala Lys Leu Thr Ser Pro Lys Arg Val Thr Ser
420 425 430

Leu Phe Ser Arg
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<212> DNA
<213> Oryza sativa

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ttattgtaaa gttctacaaa gctaatttaa aagttattgc attaacttat ttcattattac 180
aaacaagagt gtcaatggaa caatgaaaac catatgacat actataatth tgthttttatt 240
attgaaatta tataattcaa agagaataaa tccacatagc cgtaaagttc tacatgtggt 300
gcattaccaa aatatatata gcttacaaaa catgacaagc ttagtttgaa aaattgcaat 360
ccttatcaca ttgacacata aagtgagtga tgagtcataa tattatthttc ttgctaccc 420
atcatgtata tatgatagcc acaaagttac ttgatgatg atatcaaaga acattthtttag 480
gtgcacctaa cagaatatcc aaataatatg actcacttag atcataatag agcatcaagt 540
aaaactaaca ctctaaagca accgatggga aagcatctat aaatagacaa gcacaatgaa 600

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<211> 56
<212> DNA
<213> Artificial sequence

<220>
<223> primer PRM582

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<211> 52
<212> DNA
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<220>
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<213> Unknown

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<221> misc_feature
<222> 3
<223> Xaa at position 3 may be Val or Ile

<220>
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<223> Xaa at position 6 may be Ser or Ala

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<222> 7
<223> Xaa at position 7 may be Asp or Glu

<220>
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<222> 8
<223> Xaa at position 8 may be Asp or Glu

<220>
<221> misc_feature

<222> 10
<223> Xaa at positon 10 may be Lys, Arg or Thr

<400> 6

Trp Leu Xaa Glu Val Xaa Xaa Xaa Tyr Xaa Leu
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<210> 7
<211> 15
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<213> Unknown

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<223> motif 2, found in cyclin A2 proteins

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<223> Xaa at position 5 may be Val, Ile, Thr or Met

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<223> Xaa at position 6 may be Asp, Glu or Met

<220>
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<222> 8
<223> Xaa at position 8 may be Thr, Ser, His, Pro or Gly

<220>
<221> misc_feature
<222> 10
<223> Xaa at position 10 may be Arg or Leu

<220>
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<222> 11
<223> Xaa at position 11 may be Leu, Arg, Lys or Asn

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Glu Leu Thr Leu Xaa Xaa Tyr Xaa Phe Xaa Xaa Phe Leu Pro Ser
1 5 10 15

<210> 8
<211> 15
<212> PRT
<213> Arabidopsis thaliana

<400> 8

Trp Leu Val Glu Val Ser Glu Glu Tyr Lys Leu Val Ser Asp Thr
1 5 10 15

<210> 9

<211> 15

<212> PRT

<213> Arabidopsis thaliana

<400> 9

Trp	Leu	Val	Glu	Val	Ser	Asp	Asp	Tyr	Lys	Leu	Val	Pro	Asp	Thr
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<210> 10

<211> 15

<212> PRT

<213> Arabidopsis thaliana

<400> 10

Trp	Leu	Val	Glu	Val	Ser	Glu	Glu	Tyr	Thr	Leu	Ala	Ser	Asp	Thr
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<210> 11

<211> 15

<212> PRT

<213> Arabidopsis thaliana

<400> 11

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<213> Oryza sativa

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<210> 13

<211> 15

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<210> 14

<211> 15

<212> PRT

<213> Nicotiana tabacum

<400> 14

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1 5 10 15

<210> 15

<211> 15

<212> PRT

<213> Arabidopsis thaliana

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<400> 16

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<210> 17

<211> 15

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<213> Arabidopsis thaliana

<400> 17

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<210> 18

<211> 15

<212> PRT

<213> Oryza sativa

<400> 18

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1 5 10 15

<210> 19

<211> 15

<212> PRT

<213> Arabidopsis thaliana

<400> 19

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<210> 21

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<210> 22

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<213> *Arabidopsis thaliana*

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<210> 23

<211> 15

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<213> *Arabidopsis thaliana*

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<210> 24

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<213> *Oryza sativa*

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<210> 25

<211> 15

<212> PRT

<213> *Medicago*

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1 5 10 15

<210> 26
<211> 15
<212> PRT
<213> *Nicotiana tabacum*

<400> 26

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<210> 27
<211> 15
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<213> *Arabidopsis thaliana*

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1 5 10 15

<210> 28
<211> 15
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<210> 29
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<212> PRT
<213> *Arabidopsis thaliana*

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<213> *Oryza sativa*

<400> 30

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<211> 16

<212> PRT

<213> *Arabidopsis thaliana*

<400> 31

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